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* * * * * Welcome to STN International * * * * *

NEWS	1		Web Page for STN Seminar Schedule - N. America
NEWS	2	JUL 02	LMEDLINE coverage updated
NEWS	3	JUL 02	SCISEARCH enhanced with complete author names
NEWS	4	JUL 02	CHEMCATS accession numbers revised
NEWS	5	JUL 02	CA/CAPplus enhanced with utility model patents from China
NEWS	6	JUL 16	CAPplus enhanced with French and German abstracts
NEWS	7	JUL 18	CA/CAPplus patent coverage enhanced
NEWS	8	JUL 26	USPATFULL/USPAT2 enhanced with IPC reclassification
NEWS	9	JUL 30	USGENE now available on STN
NEWS	10	AUG 06	CAS REGISTRY enhanced with new experimental property tags
NEWS	11	AUG 06	BEILSTEIN updated with new compounds
NEWS	12	AUG 06	FSTA enhanced with new thesaurus edition
NEWS	13	AUG 13	CA/CAPplus enhanced with additional kind codes for granted patents
NEWS	14	AUG 20	CA/CAPplus enhanced with CAS indexing in pre-1907 records
NEWS	15	AUG 27	Full-text patent databases enhanced with predefined patent family display formats from INPADOCDB
NEWS	16	AUG 27	USPATOLD now available on STN
NEWS	17	AUG 28	CAS REGISTRY enhanced with additional experimental spectral property data
NEWS	18	SEP 07	STN AnaVist, Version 2.0, now available with Derwent World Patents Index
NEWS	19	SEP 13	FORIS renamed to SOFIS
NEWS	20	SEP 13	INPADOCDB enhanced with monthly SDI frequency
NEWS	21	SEP 17	CA/CAPplus enhanced with printed CA page images from 1967-1998
NEWS	22	SEP 17	CAPplus coverage extended to include traditional medicine patents
NEWS	23	SEP 24	EMBASE, EMBAL, and LEMBASE reloaded with enhancements
NEWS	24	OCT 02	CA/CAPplus enhanced with pre-1907 records from Chemisches Zentralblatt
NEWS EXPRESS	19	SEPTEMBER 2007:	CURRENT WINDOWS VERSION IS V8.2, CURRENT MACINTOSH VERSION IS V6.0c(ENG) AND V6.0Jc(JP), AND CURRENT DISCOVER FILE IS DATED 19 SEPTEMBER 2007.
NEWS HOURS			STN Operating Hours Plus Help Desk Availability
NEWS LOGIN			Welcome Banner and News Items
NEWS IPC8			For general information regarding STN implementation of IPC 8

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* * * * * STN Columbus * * * * *

FILE 'HOME' ENTERED AT 14:26:25 ON 17 OCT 2007

=> fil medline biosis caplus scisearch embase wpids
COST IN U.S. DOLLARS

	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	0.42	0.42

FILE 'MEDLINE' ENTERED AT 14:27:17 ON 17 OCT 2007

FILE 'BIOSIS' ENTERED AT 14:27:17 ON 17 OCT 2007
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FILE 'CAPLUS' ENTERED AT 14:27:17 ON 17 OCT 2007
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FILE 'WPIDS' ENTERED AT 14:27:17 ON 17 OCT 2007
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=> e minor-james/au

E1	4	MINOR WM F/AU
E2	1	MINOR Z/AU
E3	0	--> MINOR-JAMES/AU
E4	5	MINORA ATSUSHI/AU
E5	1	MINORA DORIYO/AU
E6	1	MINORA DORYO/AU
E7	3	MINORA G/AU
E8	7	MINORA HARUYUKI/AU
E9	4	MINORA HIDEJI/AU
E10	3	MINORA HIDEKI/AU
E11	1	MINORA HIROYUKI/AU
E12	1	MINORA HISASHI/AU

=> e minor james/au

E1	4	MINOR J W/AU
E2	13	MINOR JACOB C/AU
E3	10	--> MINOR JAMES/AU
E4	6	MINOR JAMES B/AU
E5	3	MINOR JAMES C/AU
E6	3	MINOR JAMES CRAIG/AU
E7	1	MINOR JAMES E/AU
E8	1	MINOR JAMES G/AU
E9	2	MINOR JAMES I JR/AU
E10	17	MINOR JAMES L/AU
E11	1	MINOR JAMES LYELL/AU
E12	29	MINOR JAMES M/AU

=> e3 or e12

L1 39 "MINOR JAMES"/AU OR "MINOR JAMES M"/AU

=> e minor james m?/au

E1	1	MINOR JAMES LYELL/AU
E2	29	MINOR JAMES M/AU
E3	0 -->	MINOR JAMES M?/AU
E4	10	MINOR JAMES R/AU
E5	1	MINOR JAN/AU
E6	14	MINOR JAN L/AU
E7	1	MINOR JENNIFER L/AU
E8	1	MINOR JERIS K/AU
E9	4	MINOR JESSE E/AU
E10	1	MINOR JESSIE/AU
E11	30	MINOR JESSIE E/AU
E12	3	MINOR JOHN/AU

=> dup rem l1

PROCESSING COMPLETED FOR L1

L2 33 DUP REM L1 (6 DUPLICATES REMOVED)

=> t ti l2 1-33

L2 ANSWER 1 OF 33 CAPLUS COPYRIGHT 2007 ACS on STN

TI Label integrity verification of chemical array data of labeled biopolymers

L2 ANSWER 2 OF 33 CAPLUS COPYRIGHT 2007 ACS on STN

TI Label integrity verification of chemical array data of labeled biopolymers

L2 ANSWER 3 OF 33 BIOSIS COPYRIGHT (c) 2007 The Thomson Corporation on STN

TI Methods and system for comparing data values across multiple platforms.

L2 ANSWER 4 OF 33 BIOSIS COPYRIGHT (c) 2007 The Thomson Corporation on STN

TI Methods and system for comparing data values across multiple platforms.

L2 ANSWER 5 OF 33 CAPLUS COPYRIGHT 2007 ACS on STN

TI Methods and system for comparing data values across multiple platforms

L2 ANSWER 6 OF 33 BIOSIS COPYRIGHT (c) 2007 The Thomson Corporation on STN

TI Microarray quality control.

L2 ANSWER 7 OF 33 BIOSIS COPYRIGHT (c) 2007 The Thomson Corporation on STN

TI Increased genomic resolution in microarray-based oligo CGH: Refined aberration mapping using agilent 185K arrays.

L2 ANSWER 8 OF 33 MEDLINE on STN

DUPLICATE 1

TI Microarray quality control.

L2 ANSWER 9 OF 33 CAPLUS COPYRIGHT 2007 ACS on STN

TI Treatment discovery based on comparative genomic hybridization (CGH) analysis

L2 ANSWER 10 OF 33 CAPLUS COPYRIGHT 2007 ACS on STN

TI Methods and systems for differential clustering of gene expression profiles for high throughput identification of potential functionally variant genes

L2 ANSWER 11 OF 33 CAPLUS COPYRIGHT 2007 ACS on STN

TI Statistical analysis methods for comparing gene expression profiles in tissues for diagnosis of diseases

L2 ANSWER 12 OF 33 CAPLUS COPYRIGHT 2007 ACS on STN

TI Analyzing and correcting biological assay data using a signal allocation model and applications to microarray gene expression profile studies

L2 ANSWER 13 OF 33 CAPLUS COPYRIGHT 2007 ACS on STN

TI Methods, systems and recordable media for multi-drug treatment discovery

using expression data characterizing protein pathways of diseases

L2 ANSWER 14 OF 33 CAPLUS COPYRIGHT 2007 ACS on STN

TI Feature quantitation methods and system

L2 ANSWER 15 OF 33 MEDLINE on STN

DUPLICATE 2

TI Development of a large-scale chemogenomics database to improve drug candidate selection and to understand mechanisms of chemical toxicity and action.

L2 ANSWER 16 OF 33 MEDLINE on STN

TI A survey of ovary-, testis-, and soma-biased gene expression in *Drosophila melanogaster* adults.

L2 ANSWER 17 OF 33 MEDLINE on STN

TI FlyGEM, a full transcriptome array platform for the *Drosophila* community.

L2 ANSWER 18 OF 33 CAPLUS COPYRIGHT 2007 ACS on STN

TI A survey of ovary-, testis-, and soma-biased gene expression in *Drosophila melanogaster* adults

L2 ANSWER 19 OF 33 CAPLUS COPYRIGHT 2007 ACS on STN

TI FlyGEM, a full transcriptome array platform for the *Drosophila* community

L2 ANSWER 20 OF 33 BIOSIS COPYRIGHT (c) 2007 The Thomson Corporation on STN

TI Multivariate models predict outcome to hepatitis C virus therapy at baseline and at weeks 4 and 8.

L2 ANSWER 21 OF 33 BIOSIS COPYRIGHT (c) 2007 The Thomson Corporation on STN

TI Microarray analysis of sexual dimorphism in *Drosophila*.

L2 ANSWER 22 OF 33 CAPLUS COPYRIGHT 2007 ACS on STN

TI An evaluation of the performance of cDNA microarrays for detecting changes in global mRNA expression

L2 ANSWER 23 OF 33 BIOSIS COPYRIGHT (c) 2007 The Thomson Corporation on STN

DUPLICATE 3

TI Effect of multiple freeze-thaw cycles on hepatitis B virus DNA and hepatitis C virus RNA quantification as measured with branched-DNA technology.

L2 ANSWER 24 OF 33 BIOSIS COPYRIGHT (c) 2007 The Thomson Corporation on STN

TI Impact of interferon-alpha therapy on growth of children with chronic hepatitis B virus disease.

L2 ANSWER 25 OF 33 CAPLUS COPYRIGHT 2007 ACS on STN

TI Assessment of hepatitis C virus RNA stability in serum by the Quantiplex branched DNA assay

L2 ANSWER 26 OF 33 BIOSIS COPYRIGHT (c) 2007 The Thomson Corporation on STN

DUPLICATE 4

TI Assessment of hepatitis B virus DNA stability in serum by the chiron quantiplex branched-DNA assay.

L2 ANSWER 27 OF 33 CAPLUS COPYRIGHT 2007 ACS on STN

TI Infrared spectra of amorphous and crystalline poly(tetrafluoroethylene)

L2 ANSWER 28 OF 33 CAPLUS COPYRIGHT 2007 ACS on STN

TI Optimization of solvent strength and selectivity for reversed-phase liquid chromatography using an interactive mixture-design statistical technique

L2 ANSWER 29 OF 33 CAPLUS COPYRIGHT 2007 ACS on STN
 TI Optimization of solvent strength and selectivity for reversed-phase liquid chromatography using an interactive mixture-design statistical technique

L2 ANSWER 30 OF 33 CAPLUS COPYRIGHT 2007 ACS on STN
 TI Analytic self-consistent-field wave functions for the (3d)(4s) configuration of the transition-metal ions

L2 ANSWER 31 OF 33 CAPLUS COPYRIGHT 2007 ACS on STN
 TI Variational calculation of the multiplet spacings in the (3d)² electron configurations

L2 ANSWER 32 OF 33 CAPLUS COPYRIGHT 2007 ACS on STN
 TI Two-electron correlation effects in Hartree-Fock atomic systems

L2 ANSWER 33 OF 33 CAPLUS COPYRIGHT 2007 ACS on STN
 TI Variational calculation of the multiplet spacings in the carbon isoelectronic sequence

=> d ibib abs l2 1,3,6,7,9-17, 20-25,27,28, 30-33

L2 ANSWER 1 OF 33 CAPLUS COPYRIGHT 2007 ACS on STN
 ACCESSION NUMBER: 2007:534421 CAPLUS
 DOCUMENT NUMBER: 146:478319
 TITLE: Label integrity verification of chemical array data of labeled biopolymers
 INVENTOR(S): Minor, James M.
 PATENT ASSIGNEE(S): USA
 SOURCE: U.S. Pat. Appl. Publ., 23pp.
 CODEN: USXXCO
 DOCUMENT TYPE: Patent
 LANGUAGE: English
 FAMILY ACC. NUM. COUNT: 1
 PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2007111219	A1	20070517	US 2005-283453	20051117
PRIORITY APPLN. INFO.:			US 2005-283453	20051117

AB Methods, systems and computer readable media for checking label integrity of labeled biopolymers in a sample assayed by chemical array anal. A sample is divided into equal aliquots. At least first and second labels are incorporated into biopolymers contained in first and second aliquots of the equal aliquots, resp. The labels are added to the aliquots in amts. expected to incorporate into the biopolymers of the resp. aliquots to produce signals of proportional quantity when read from probes on a chemical array designed to couple with biopolymers of the aliquots. The aliquots are then combined into a single, multi-labeled sample having at least first-labeled biopolymers and second-labeled biopolymers. The multi-labeled sample is hybridized with probes on a chemical array. Signal values are read from the probes on the chemical array bound to labeled biopolymers from the multi-labeled sample. Comparisons are made between signal values from probes bound to biopolymer having the first label incorporated therein (first-labeled signal values) and signal values from the same probes bound to biopolymers having the second label incorporated therein (second-labeled signal values), resp., from which it is determined that label integrity is of acceptable quality if divergence between the first-labeled signal values and the second-labeled signal values is less than a predetd. threshold value.

L2 ANSWER 3 OF 33 BIOSIS COPYRIGHT (c) 2007 The Thomson Corporation on STN

ACCESSION NUMBER: 2006:650371 BIOSIS
DOCUMENT NUMBER: PREV200600661721
TITLE: Methods and system for comparing data values across multiple platforms.
AUTHOR(S): Anonymous; Minor, James M. [Inventor]
CORPORATE SOURCE: Los Altos, CA USA
ASSIGNEE: Agilent Technologies Inc
PATENT INFORMATION: US 07072806 20060704
SOURCE: Official Gazette of the United States Patent and Trademark Office Patents, (JUL 4 2006)
CODEN: OGUPE7. ISSN: 0098-1133.
DOCUMENT TYPE: Patent
LANGUAGE: English
ENTRY DATE: Entered STN: 29 Nov 2006
Last Updated on STN: 29 Nov 2006

AB Methods, systems and computer readable media for imposing monotonic consistency among results of multiple platforms measuring the same specific property for the same/equivalent series of samples, to provide viable comparisons of sensitivity and precision among the platforms as well as provide useful conversion formulas among the platforms to ensure equivalent quantitation.

L2 ANSWER 6 OF 33 BIOSIS COPYRIGHT (c) 2007 The Thomson Corporation on STN
ACCESSION NUMBER: 2007:234303 BIOSIS
DOCUMENT NUMBER: PREV200700234913
TITLE: Microarray quality control.
AUTHOR(S): Minor, James M. [Reprint Author]
CORPORATE SOURCE: Agilent Technol Inc, Santa Clara, CA USA
SOURCE: Kimmel, A [Editor]; Oluver, B [Editor]. Methods Enzymol., (2006) pp. 233-255. Methods in Enzymology. Publisher: ELSEVIER ACADEMIC PRESS INC, 525 B STREET, SUITE 1900, SAN DIEGO, CA 92101-4495 USA. Series: METHODS IN ENZYMOLOGY.
CODEN: MENZAU. ISSN: 0076-6879. ISBN: 978-0-12-182816-5(H).
DOCUMENT TYPE: Book; (Book Chapter)
LANGUAGE: English
ENTRY DATE: Entered STN: 11 Apr 2007
Last Updated on STN: 11 Apr 2007

AB Physically separated groups of specific sequences (probes) provide useful high through put (HTP) measurements for the amount of selected DNA/RNA sequences in a biological target sample. Unfortunately, these measurements are impacted by various technical sources, such as platform production factors, target preparation processes, hybridization method/conditions, and signal-extraction devices and methods. Given the typically huge population of signals, statistical methods are especially effective at estimation and removal of such technical distortions (Churchill, 2002; Kerr et al., 2000; Yue et al., 2001), as well as providing metrics for computer-based quality control (QC), for example, autoQC (Minor et al., 2002a). This chapter reviews statistical procedures that have been validated by successful applications in both large-scale commercial ventures (Ganter et al., 2005) and individual research studies (Parisi et al., 2003, 2004) involving HTP projects. This chapter focuses on methods for spatially distributed

L2 ANSWER 7 OF 33 BIOSIS COPYRIGHT (c) 2007 The Thomson Corporation on STN
ACCESSION NUMBER: 2006:585991 BIOSIS
DOCUMENT NUMBER: PREV200600596617
TITLE: Increased genomic resolution in microarray-based oligo CGH: Refined aberration mapping using agilent 185K arrays.
AUTHOR(S): Roberts, Douglas N. [Reprint Author]; Giles, Shane; Leproust, Eric M.; Sampas, Nick; Shchegrova, Svetlana; Minor, James; Tsang, Peter; Curry, Bo; Bruhn, Laurakay; Webb, Peter

CORPORATE SOURCE: Agilent Technol, Palo Alto, CA USA
 SOURCE: Proceedings of the American Association for Cancer Research
 Annual Meeting, (APR 2006) Vol. 47, pp. 618.
 Meeting Info.: 97th Annual Meeting of the
 American-Association-for-Cancer-Research (AACR).
 Washington, DC, USA. April 01 -05, 2006. Amer Assoc Canc
 Res.
 ISSN: 0197-016X.
 DOCUMENT TYPE: Conference; (Meeting)
 Conference; Abstract; (Meeting Abstract)
 LANGUAGE: English
 ENTRY DATE: Entered STN: 8 Nov 2006
 Last Updated on STN: 8 Nov 2006

L2 ANSWER 9 OF 33 CAPLUS COPYRIGHT 2007 ACS on STN
 ACCESSION NUMBER: 2005:1335580 CAPLUS
 DOCUMENT NUMBER: 144:46258
 TITLE: Treatment discovery based on comparative genomic
 hybridization (CGH) analysis
 INVENTOR(S): Minor, James M.; Woo, Wilson
 PATENT ASSIGNEE(S): USA
 SOURCE: U.S. Pat. Appl. Publ., 20 pp., Cont.-in-part of U.S.
 Ser. No. 640,081.
 CODEN: USXXCO
 DOCUMENT TYPE: Patent
 LANGUAGE: English
 FAMILY ACC. NUM. COUNT: 2
 PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2005282227	A1	20051222	US 2005-215483	20050830
US 2005037363	A1	20050217	US 2003-640081	20030813
PRIORITY APPLN. INFO.:			US 2003-640081	A2 20030813

AB Methods, systems and computer readable media for discovering a combination of treatments to reduce the progress of, or eliminate a tissue malady, are provided. The methods include the steps of: (a) measuring gene expression values of sample of tissue exhibiting the tissue malady and reference sample tissue that does not exhibit the malady, using CGH array designed to measure gene sequences and possible variations in gene sequences attributable to the malady; (b) generating gene expression signatures from differential expression values of ratios of the measured gene expression values between the sample exhibiting the malady and the reference sample, across all samples, resp.; (c) treating the tissue sample exhibiting the malady with a treatment; (d) measuring a treatment-response value with respect to each of the tissue samples treated, as effected by the treatment; (e) generating a phenotypic signature representing the treatment-response values of each of the tissue samples treated; (f) repeating steps (c)-(e) with a different treatment so that multiple phenotypic signatures have been generated for multiple treatments; (g) performing a clustering operation based on the gene expression signatures of the differential expression levels and the phenotypic signatures of the treatment-response values together; and (h) selecting treatments by identifying the treatment-response phenotypic signatures caused by those treatments. In addition, embodiments of the present invention further relate to computer readable media or computer program products that include program instructions and/or data (including data structures) for performing various computer-implemented operations. The present invention is a forward-looking way of choosing and predicting specific combinations of treatments to test, e.g., using high-throughput (HTP) screening of treatment combinations, and as such, greatly reduces the time to finding successful combinations, which currently have only been discovered accidentally, through hindsight and experiences gained through individual

treatments. The treatments identified are targeted to the genes involved in the disease process/malady. Because of this, the chances of significant side effects are reduced. A technique for excluding potential treatments may also be carried out. One example of such an exclusion technique is to generate phenotypic signature representing treatment-response values of each of the tissue samples exhibiting the malady, resultant from treating the tissue samples exhibiting the malady, with treatment having known undesirable characteristics (e.g., is toxic to normal tissues, or ineffective, or has other undesirable side effects, etc.) for treatment of the tissues exhibiting the malady, using the techniques described above.

L2 ANSWER 10 OF 33 CAPLUS COPYRIGHT 2007 ACS on STN

ACCESSION NUMBER: 2005:1154196 CAPLUS

DOCUMENT NUMBER: 143:405367

TITLE: Methods and systems for differential clustering of gene expression profiles for high throughput identification of potential functionally variant genes

INVENTOR(S): Minor, James M.

PATENT ASSIGNEE(S): USA

SOURCE: U.S. Pat. Appl. Publ., 18 pp.

CODEN: USXXCO

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2005240357	A1	20051027	US 2004-831866	20040426
PRIORITY APPLN. INFO.:			US 2004-831866	20040426

AB The present invention provides methods, systems and computer readable media for high throughput identification of potential functionally variant genes. Gene expression response profiles are generated for various sets of the samples and then differentially clustered across such sets to observe genes whose expression response profiles change cluster membership going from one set to another. Statistical anal. is performed with regard to the change from one cluster membership to another to determine whether the change from one cluster membership to another is statistically significant. If the change is determined to be statistically significant, the gene represented by the gene expression response profiles having been analyzed is identified as being a potential functionally variant gene. The nature of the function change may also be identified by the present systems, methods and computer readable media. The cluster emphasis is on the synchronization of profile trend variations rather than on shifts in expression levels. The present invention further covers forwarding a result, transmitting data representing a result and/or receiving a result obtained from any of the methods described herein.

L2 ANSWER 11 OF 33 CAPLUS COPYRIGHT 2007 ACS on STN

ACCESSION NUMBER: 2005:1103245 CAPLUS

DOCUMENT NUMBER: 143:366726

TITLE: Statistical analysis methods for comparing gene expression profiles in tissues for diagnosis of diseases

INVENTOR(S): Minor, James M.

PATENT ASSIGNEE(S): USA

SOURCE: U.S. Pat. Appl. Publ., 23 pp.

CODEN: USXXCO

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2005227221	A1	20051013	US 2004-821829	20040409
PRIORITY APPLN. INFO.:			US 2004-821829	20040409

AB The present invention relates to statistical anal. methods for comparing gene expression profiles in tissues for diagnosis of diseases. Computer readable media for validating or calibrating a plotted curve of sorted p-values are provided. Still further, methods, systems and computer readable media are provided for distinguishing differentially expressed genes based on plotting expression levels and replicates derived from one or more genes in one sample against corresponding expression levels and replicated derived from one or more genes in a second sample.

L2 ANSWER 12 OF 33 CAPLUS COPYRIGHT 2007 ACS on STN

ACCESSION NUMBER: 2005:570559 CAPLUS

DOCUMENT NUMBER: 143:93627

TITLE: Analyzing and correcting biological assay data using a signal allocation model and applications to microarray gene expression profile studies

INVENTOR(S): Minor, James

PATENT ASSIGNEE(S): USA

SOURCE: U.S. Pat. Appl. Publ., 10 pp.

CODEN: USXXCO

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2005143933	A1	20050630	US 2002-167119	20020610
WO 2003091845	A2	20031106	WO 2003-US12584	20030423
WO 2003091845	A3	20040401		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

AU 2003234191	A1	20031110	AU 2003-234191	20030423
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US 7248973	B2	20070724	US 2005-198362	20050804
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PRIORITY APPLN. INFO.:

US 2002-375251P	P	20020423
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US 2003-422570	A2	20030423
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WO 2003-US12584	W	20030423
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US 2004-26484	A2	20041230
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AB Data from a biol. assay are analyzed and corrected to deconvolve and estimate the

expression of a target material using the measured signals from a target probe and on or more homologous probes. The expressions of target and non-target material in a biol. sample are allocated to the measured signals of multiple probes. The SIAM model is used to correct the biol. assay data to obtain more accurate results for the true expression. In particular, the SIAM model can be used in analyzing microarray data, such as gene expression profile data.

L2 ANSWER 13 OF 33 CAPLUS COPYRIGHT 2007 ACS on STN

ACCESSION NUMBER: 2005:140656 CAPLUS

DOCUMENT NUMBER: 142:212296

TITLE: Methods, systems and recordable media for multi-drug treatment discovery using expression data characterizing protein pathways of diseases
 INVENTOR(S): Minor, James M.
 PATENT ASSIGNEE(S): USA
 SOURCE: U.S. Pat. Appl. Publ., 22 pp.
 CODEN: USXXCO
 DOCUMENT TYPE: Patent
 LANGUAGE: English
 FAMILY ACC. NUM. COUNT: 2
 PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2005037363	A1	20050217	US 2003-640081	20030813
WO 2005017804	A2	20050224	WO 2004-US26366	20040813
WO 2005017804	A3	20060323		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW
 RW: AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG, BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

US 200528227 A1 20051222 US 2005-215483 20050830
 PRIORITY APPLN. INFO.: US 2003-640081 A 20030813

AB Methods, systems and recordable media are described for using expression data characterizing protein pathways of diseases to produce phase relationships between treatment responses of diseased tissues to treatments applied thereto and expression profiles of the diseased tissues as measured when untreated. Methods, systems and recordable media are also described for augmenting an original or existing treatment or treatment combination with one or more treatments that cover gene activity of a disease not addressed by the original/existing treatment. Application to screening treatments on lung cancer tissues are illustrated.

L2 ANSWER 14 OF 33 CAPLUS COPYRIGHT 2007 ACS on STN

ACCESSION NUMBER: 2005:340267 CAPLUS
 DOCUMENT NUMBER: 142:375672
 TITLE: Feature quantitation methods and system
 INVENTOR(S): Minor, James M.
 PATENT ASSIGNEE(S): Agilent Technologies, Inc., USA
 SOURCE: Brit. UK Pat. Appl., 55 pp.
 CODEN: BAXXDU

DOCUMENT TYPE: Patent
 LANGUAGE: English
 FAMILY ACC. NUM. COUNT: 1
 PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
GB 2407157	A	20050420	GB 2004-22642	20041012
GB 2407157	B	20060614		

PRIORITY APPLN. INFO.: US 2003-685135 A 20031014

AB Methods, systems and recordable media are described for accurately reading and identifying high quality signals from a microarray feature. Signals may be identified and used regardless of their geog./geometric locations and patterns within the feature zone. Output signals from a chemical

microarray image are given rank order according to signal magnitude and a subset identified which are representative of the quality signals.
REFERENCE COUNT: 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 15 OF 33 MEDLINE on STN DUPLICATE 2
ACCESSION NUMBER: 2005483922 MEDLINE
DOCUMENT NUMBER: PubMed ID: 16005536
TITLE: Development of a large-scale chemogenomics database to improve drug candidate selection and to understand mechanisms of chemical toxicity and action.
AUTHOR: Ganter Brigitte; Tugendreich Stuart; Pearson Cecelia I; Ayanoglu Eser; Baumhueter Susanne; Bostian Keith A; Brady Lindsay; Browne Leslie J; Calvin John T; Day Gwo-Jen; Breckenridge Naiomi; Dunlea Shane; Eynon Barrett P; Furness L Mike; Ferng Joe; Fielden Mark R; Fujimoto Susan Y; Gong Li; Hu Christopher; Idury Radha; Judo Michael S B; Kolaja Kyle L; Lee May D; McSorley Christopher; Minor James M; Nair Ramesh V; Natsoulis Georges; Nguyen Peter; Nicholson Simone M; Pham Hang; Roter Alan H; Sun Dongxu; Tan Siqi; Thode Silke; Tolley Alexander M; Vladimirova Antoaneta; Yang Jian; Zhou Zhiming; Jarnagin Kurt
CORPORATE SOURCE: Iconix Pharmaceuticals, 325 E. Middlefield Road, Mountain View, CA 94043, USA.. bganter@iconixpharm.com
SOURCE: Journal of biotechnology, (2005 Sep 29) Vol. 119, No. 3, pp. 219-44.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200601
ENTRY DATE: Entered STN: 13 Sep 2005
Last Updated on STN: 7 Jan 2006
Entered Medline: 6 Jan 2006

AB Successful drug discovery requires accurate decision making in order to advance the best candidates from initial lead identification to final approval. Chemogenomics, the use of genomic tools in pharmacology and toxicology, offers a promising enhancement to traditional methods of target identification/validation, lead identification, efficacy evaluation, and toxicity assessment. To realize the value of chemogenomics information, a contextual database is needed to relate the physiological outcomes induced by diverse compounds to the gene expression patterns measured in the same animals. Massively parallel gene expression characterization coupled with traditional assessments of drug candidates provides additional, important mechanistic information, and therefore a means to increase the accuracy of critical decisions. A large-scale chemogenomics database developed from in vivo treated rats provides the context and supporting data to enhance and accelerate accurate interpretation of mechanisms of toxicity and pharmacology of chemicals and drugs. To date, approximately 600 different compounds, including more than 400 FDA approved drugs, 60 drugs approved in Europe and Japan, 25 withdrawn drugs, and 100 toxicants, have been profiled in up to 7 different tissues of rats (representing over 3200 different drug-dose-time-tissue combinations). Accomplishing this task required evaluating and improving a number of in vivo and microarray protocols, including over 80 rigorous quality control steps. The utility of pairing clinical pathology assessments with gene expression data is illustrated using three anti-neoplastic drugs: carmustine, methotrexate, and thioguanine, which had similar effects on the blood compartment, but diverse effects on hepatotoxicity. We will demonstrate that gene expression events monitored in the liver can be used to predict pathological events occurring in that tissue as well as in hematopoietic

tissues.

L2 ANSWER 16 OF 33 MEDLINE on STN
ACCESSION NUMBER: 2004286882 MEDLINE
DOCUMENT NUMBER: PubMed ID: 15186491
TITLE: A survey of ovary-, testis-, and soma-biased gene expression in *Drosophila melanogaster* adults.
AUTHOR: Parisi Michael; Nuttall Rachel; Edwards Pamela; Minor James; Naiman Daniel; Lu Jining; Doctolero Michael; Vainer Marina; Chan Cathy; Malley James; Eastman Scott; Oliver Brian
CORPORATE SOURCE: Laboratory of Cellular and Developmental Biology, National Institute of Diabetes and Digestive and Kidney Diseases, National Institutes of Health, Department of Health and Human Services, Bethesda, MD 20892, USA..
CONTRACT NUMBER: Z01 DK015600-10 (NIDDK)
SOURCE: Genome biology, (2004) Vol. 5, No. 6, pp. R40. Electronic Publication: 2004-06-01.
PUB. COUNTRY: England: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200410
ENTRY DATE: Entered STN: 10 Jun 2004
Last Updated on STN: 13 Oct 2004
Entered Medline: 12 Oct 2004

AB BACKGROUND: Sexual dimorphism results in the formation of two types of individuals with specialized reproductive roles and is most evident in the germ cells and gonads. RESULTS: We have undertaken a global analysis of transcription between the sexes using a 31,464 element FlyGEM microarray to determine what fraction of the genome shows sex-biased expression, what tissues express these genes, the predicted functions of these genes, and where these genes map onto the genome. Females and males (both with and without gonads), dissected testis and ovary, females and males with genetically ablated germlines, and sex-transformed flies were sampled. CONCLUSIONS: Using any of a number of criteria, we find extensive sex-biased expression in adults. The majority of cases of sex differential gene expression are attributable to the germ cells. There is also a large class of genes with soma-biased expression. There is little germline-biased expression indicating that nearly all genes with germline expression also show sex-bias. Monte Carlo simulations show that some genes with sex-biased expression are non-randomly distributed in the genome.

L2 ANSWER 17 OF 33 MEDLINE on STN
ACCESSION NUMBER: 2004113877 MEDLINE
DOCUMENT NUMBER: PubMed ID: 15003122
TITLE: FlyGEM, a full transcriptome array platform for the *Drosophila* community.
AUTHOR: Johnston Rick; Wang Bruce; Nuttall Rachel; Doctolero Michael; Edwards Pamela; Lu Jining; Vainer Marina; Yue Huibin; Wang Xinhao; Minor James; Chan Cathy; Lash Alex; Goralski Thomas; Parisi Michael; Oliver Brian; Eastman Scott
CORPORATE SOURCE: Incyte Genomics, Palo Alto, CA 94304, USA.
CONTRACT NUMBER: Z01 DK015600-10 (NIDDK)
SOURCE: Genome biology, (2004) Vol. 5, No. 3, pp. R19. Electronic Publication: 2004-02-26.
PUB. COUNTRY: England: United Kingdom

DOCUMENT TYPE: (COMPARATIVE STUDY)
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200410
ENTRY DATE: Entered STN: 9 Mar 2004
Last Updated on STN: 7 Oct 2004
Entered Medline: 6 Oct 2004

AB We have constructed a DNA microarray to monitor expression of predicted genes in *Drosophila*. By using homotypic hybridizations, we show that the array performs reproducibly, that dye effects are minimal, and that array results agree with systematic northern blotting. The array gene list has been extensively annotated and linked-out to other databases. Incyte and the NIH have made the platform available to the community via academic microarray facilities selected by an NIH committee.

L2 ANSWER 20 OF 33 BIOSIS COPYRIGHT (c) 2007 The Thomson Corporation on STN.

ACCESSION NUMBER: 2004:134246 BIOSIS
DOCUMENT NUMBER: PREV200400132312
TITLE: Multivariate models predict outcome to hepatitis C virus therapy at baseline and at weeks 4 and 8.

AUTHOR(S): Peignoux, Michele Martinot [Reprint Author]; Comanor, Lorraine; Minor, James; Ripault, Marie Pierre [Reprint Author]; Boyer, Natalie [Reprint Author]; Castelnau, Corinne [Reprint Author]; Guily, Nathalie [Reprint Author]; Hendricks, David; Marcellin, Patrick [Reprint Author]

CORPORATE SOURCE: INSERM U481, Clichy, France
SOURCE: Hepatology, (October 2003) Vol. 38, No. 4 Suppl. 1, pp. 745A. print.
Meeting Info.: 54th Annual Meeting of the American Association for the Study of Liver Diseases. Boston, MA, USA. October 24-28, 2003. American Association for the Study of Liver Diseases.
ISSN: 0270-9139 (ISSN print).

DOCUMENT TYPE: Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)

LANGUAGE: English

ENTRY DATE: Entered STN: 10 Mar 2004
Last Updated on STN: 10 Mar 2004

AB Background: Given the current burden of hepatitis C virus (HCV) therapy, physicians have been seeking a reliable early stopping rule for patients undergoing pegylated combination therapy who will be non-responders. We used data from 174 chronically infected HCV patients to develop multivariate models (MM) to predict non-response (NR), sustained response (SR) and relapse (RR) from information available in the first 8 weeks of therapy. We compared information from univariate models (UMs), based solely on quantitative or qualitative HCV RNA information, with that derived from MMs. Materials and Methods: 174 chronically infected HCV patients (94 treatment naive and 80 previously failed) were treated with pegylated interferon alpha-2b 1.5 mg/kg/week plus ribavirin 800-1200 mg/day. Naive genotype 1 or 4 patients and previously failed patients were treated for 48 weeks; patients with HCV genotype 2, 3, or 5, for 24 weeks. SR was defined as undetectable HCV RNA by the VERSANTR HCV RNA Qualitative Assay (TMA) (Bayer Diagnostics) at end-of-treatment (EOT) and follow-up at week 24 (FU24). Serum HCV RNA was quantified by the VERSANTR HCV RNA 3.0 Assay (bDNA) (Bayer Diagnostics; at baseline, weeks 4, 8, EOT, and FU24. If the HCV RNA concentration was below 615 IU/mL, specimens were then tested by HCV Qual (TMA) (limit of detection ltoreq9.6 IU/mL.) Univariate models: Baseline UM utilized a prediction threshold of 6.14 log10 copies/mL to predict outcome. Week 4 and 8 UM used a 2 log10 drop rule (gtoreq or <2 log drop in viral load from baseline; UM2 log) or

clearance of virus or lack thereof by the HCV Qual (TMA) (UM TMA). Multivariate models: MM employ ordinal regression with similarity least squares technology to assign a given outcome to the highest probability of response. Different numbers of "critical patients" (n=33-57) were used to derive the models using design of experiment and functional techniques for each time point; the models were then tested on the remaining patients (n>110). Model variables included: HCV RNA concentrations at baseline and weeks 4 and 8, gender, age, baseline ALT, inflammatory and fibrosis scores, genotype and treatment status (naive or previous therapy). Results: The comparative sensitivity specificity, positive and negative predictive values (PPV and NPV) at for the UMs and MMs are given. Baseline and week 4 models combined NRs and RRs into non-responder group, whereas week 8 model correctly separated SRs, RRs, and NRs. Prediction of SR or NR at Baseline and Weeks 4 and 8 of Therapy percent of SR identified by model; 2 percent of non-responders identified by model; 3 percent of SR predicted by model who are true SR; 4 percent of NR predicted by model who are true NR; 5gtoreq or <6.14 log10 c/mL; 6gtoreq or <2 log10 change in c/mL; 7 HCV RNA detected or not detected by TMA Conclusions: At each time point, the multivariate models demonstrates greater sensitivity, specificity, PPV and NPV than do the univariate models. Multivariate models can identify SR and non SR (NR and RR as one group) at baseline and week 4. By week 8 multivariate models can correctly identify SR, RR, and NR. The 100% prediction of non-response by the multivariate model at week 8 with the 97% NPV of < a 2 log drop suggests a week 8 stopping rule could be employed.

L2 ANSWER 21 OF 33 BIOSIS COPYRIGHT (c) 2007 The Thomson Corporation on STN
 ACCESSION NUMBER: 2003:422403 BIOSIS
 DOCUMENT NUMBER: PREV200300422403
 TITLE: Microarray analysis of sexual dimorphism in Drosophila.
 AUTHOR(S): Parisi, Michael J. [Reprint Author]; Nuttall, Rachel; Lu, Jining [Reprint Author]; Chan, Cathleen; Vainer, Marina; Minor, James; Lash, Alex; Eastman, Scott; Malley, James [Reprint Author]; Naiman, Daniel; Oliver, Brian [Reprint Author]
 CORPORATE SOURCE: National Institutes of Health, Bethesda, MD, USA
 SOURCE: Developmental Biology, (July 15 2003) Vol. 259, No. 2, pp. 528. print.
 Meeting Info.: 62nd Annual Meeting of the Society for Developmental Biology held Jointly with the International Society of Developmental Biologists. Boston, MA, USA. July 30-August 03, 2003. International Society of Developmental Biologists; Society for Developmental Biology.
 ISSN: 0012-1606 (ISSN print).
 DOCUMENT TYPE: Conference; (Meeting)
 Conference; Abstract; (Meeting Abstract)
 LANGUAGE: English
 ENTRY DATE: Entered STN: 17 Sep 2003
 Last Updated on STN: 17 Sep 2003

L2 ANSWER 22 OF 33 CAPLUS COPYRIGHT 2007 ACS on STN
 ACCESSION NUMBER: 2001:334893 CAPLUS
 DOCUMENT NUMBER: 136:48990
 TITLE: An evaluation of the performance of cDNA microarrays for detecting changes in global mRNA expression
 AUTHOR(S): Yue, Huibin; Eastman, P. Scott; Wang, Bruce B.; Minor, James; Doctolero, Michael H.; Nuttall, Rachel L.; Stack, Robert; Becker, John W.; Montgomery, Julie R.; Vainer, Marina; Johnston, Rick
 CORPORATE SOURCE: Advanced Research Group, Incyte Genomics, Fremont, CA, 94555, USA
 SOURCE: Nucleic Acids Research (2001), 29(8), e41/1-e41/9

CODEN: NARHAD; ISSN: 0305-1048
PUBLISHER: Oxford University Press
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The cDNA microarray is one technol. approach that has the potential to accurately measure changes in global mRNA expression levels. We report an assessment of an optimized cDNA microarray platform to generate accurate, precise and reliable data consistent with the objective of using microarrays as an acquisition platform to populate gene expression databases. The study design consisted of two independent evaluations with 70 arrays from two different manufactured lots and used three human tissue sources as samples: placenta, brain and heart. Overall signal response was linear over three orders of magnitude and the sensitivity for any element was estimated to be 2 pg mRNA. The calculated coefficient of variation for

differential expression for all non-differentiated elements was 12-14% across the entire signal range and did not vary with array batch or tissue source. The min. detectable fold change for differential expression was 1.4. Accuracy, in terms of bias (observed minus expected differential expression ratio), was less than one part in 10,000 for all non-differentiated elements. The results presented in this report demonstrate the reproducible performance of the cDNA microarray technol. platform and the methods provide a useful framework for evaluating other technologies that monitor changes in global mRNA expression.

REFERENCE COUNT: 17 THERE ARE 17 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 23 OF 33 BIOSIS COPYRIGHT (c) 2007 The Thomson Corporation on
STN DUPLICATE 3

ACCESSION NUMBER: 1999:518874 BIOSIS
DOCUMENT NUMBER: PREV199900518874
TITLE: Effect of multiple freeze-thaw cycles on hepatitis B virus DNA and hepatitis C virus RNA quantification as measured with branched-DNA technology.
AUTHOR(S): Krajden, Mel [Reprint author]; Minor, James M.; Rifkin, Oretta; Comanor, Lorraine
CORPORATE SOURCE: BC Center for Disease Control, 655 W. 12th Ave., Vancouver, BC, V5Z 4R4, Canada
SOURCE: Journal of Clinical Microbiology, (June, 1999) Vol. 37, No. 6, pp. 1683-1686. print.
CODEN: JCMIDW. ISSN: 0095-1137.
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 3 Dec 1999
Last Updated on STN: 3 Dec 1999

AB Quantification of hepatitis B virus (HBV) DNA and hepatitis C virus (HCV) RNA often is performed in specimens that have been frozen and thawed more than once. To ensure optimal therapeutic and prognostic value, it is important to establish whether viral load measurements are affected by repeated freeze-thaw (FT) cycles. We therefore evaluated the effect of multiple FT cycles on HBV DNA and HCV RNA quantification by testing serum specimens subjected to one (baseline), two, four, and eight FT cycles with the appropriate Chiron Quantiplex assay. Linear regression analysis showed minor increases of 1.7% per FT cycle for both HBV DNA and HCV RNA. The rise in HCV RNA levels was more pronounced among low-concentration samples, since further analysis revealed an increase of 3.2% per FT cycle among samples with 0.2 to 3.86 Meq of HCV RNA per ml. Given that the coefficient of variation for the Quantiplex assays is generally 10 to 15%, the minor increases in HBV DNA and HCV RNA levels with progressive FT cycles for the specimens tested were recognized only because analysis of variance revealed a statistically significant trend ($P < 0.05$). Due to the minor statistical trend, the clinical impact for individual patient specimens is likely to be limited, but it may deserve further study. In

conclusion, the concentration of HBV DNA and HCV RNA in serum specimens subjected to up to eight short-term FT cycles was stable.

L2 ANSWER 24 OF 33 BIOSIS COPYRIGHT (c) 2007 The Thomson Corporation on STN

ACCESSION NUMBER: 1999:499837 BIOSIS
DOCUMENT NUMBER: PREV199900499837
TITLE: Impact of interferon-alpha therapy on growth of children with chronic hepatitis B virus disease.
AUTHOR(S): Comanor, Lorraine [Reprint author]; Minor, James [Reprint author]; Conjeevaram, Hari S.; Roberts, Eve A.; Alvarez, Fernando; Bern, Elana; Goyens, Phillipe; Rosenthal, Philip; Lachaux, Alain; Shelton, Mark; Sarles, Jacques; Sokal, Etienne M.
CORPORATE SOURCE: Bayer Diagnostics, Emeryville, CA, USA
SOURCE: Hepatology, (Oct., 1999) Vol. 30, No. 4 PART 2, pp. 344A. print.
Meeting Info.: 50th Annual Meeting and Postgraduate Courses of the American Association for the Study of Liver Diseases. Dallas, Texas, USA. November 5-9, 1999. American Association for the Study of Liver Diseases.
CODEN: HPTLD9. ISSN: 0270-9139.
DOCUMENT TYPE: Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LANGUAGE: English
ENTRY DATE: Entered STN: 23 Nov 1999
Last Updated on STN: 23 Nov 1999

L2 ANSWER 25 OF 33 CAPLUS COPYRIGHT 2007 ACS on STN

ACCESSION NUMBER: 1999:809396 CAPLUS
DOCUMENT NUMBER: 132:290599
TITLE: Assessment of hepatitis C virus RNA stability in serum by the Quantiplex branched DNA assay
AUTHOR(S): Krajden, Mel; Minor, James M.; Zhao, Jiu; Rifkin, Oretta; Comanor, Lorraine
CORPORATE SOURCE: Department of Laboratory Medicine and Pathology, The Toronto Hospital and Toronto Medical Laboratories, Toronto, ON, Can.
SOURCE: Journal of Clinical Virology (1999), 14(2), 137-143
CODEN: JCVIFB; ISSN: 1386-6532
PUBLISHER: Elsevier Science Ireland Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Objectives: Quantification of hepatitis C virus (HCV) RNA in serum is used to assess the probability of treatment response and to monitor antiviral therapy. Since serum specimens often are shipped to central sites for HCV RNA testing, it is important to define conditions that preserve HCV RNA integrity. Methods: We evaluated the stability of HCV RNA in 25 previously frozen (PF) and 11 fresh, never previously frozen (NPF) specimens subjected to handling and short-term storage conditions that mimic those encountered during interlab. shipping. All sera were separated within 4 h collection. PF samples covering a .apprx. 3 log₁₀ HCV RNA dynamic range were thawed, divided into aliquots, incubated at 4, 23, and 37° (± 1.5°) for 24, 48, 72 and 96 h (± 2 h), and then refrozen at - 70° prior to testing with the Quantiplex HCV RNA 2.0 assay. Eleven NPF samples were stored at - 70, - 20, and 4° (± 1.5°) for up to 1 mo prior to testing. Results: Linear regression anal. showed no HCV RNA degradation in PF specimens kept at 4° over 4 days. However, HCV RNA levels in PF specimens decreased over 4 days by 20 and 105% at 23 and 37°, resp. Three independent statistical methods showed that the probability of specimen failure in PF specimens, defined as a loss of 20% or more of HCV RNA, was lowest at 4° and increased with increasing temperature The HCV RNA quantification of the 11 NPF

specimens stored at 4° was similar to their frozen controls.

Conclusion: HCV RNA in separated serum specimens is stable for at least 4 days at 4°.

REFERENCE COUNT: 18 THERE ARE 18 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 27 OF 33 CAPLUS COPYRIGHT 2007 ACS on STN

ACCESSION NUMBER: 1985:524162 CAPLUS

DOCUMENT NUMBER: 103:124162

TITLE: Infrared spectra of amorphous and crystalline poly(tetrafluoroethylene)

AUTHOR(S): Starkweather, Howard W., Jr.; Ferguson, Raymond C.; Chase, D. Bruce; Minor, James M.

CORPORATE SOURCE: Cent. Res. Dev. Dep., E. I. du Pont de Nemours and Co., Wilmington, DE, 19898, USA

SOURCE: Macromolecules (1985), 18(9), 1684-6

CODEN: MAMOBX; ISSN: 0024-9297

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Attenuated-total-reflectance IR spectral data for crystalline and amorphous PTFE [9002-84-0] were treated by two-component factor anal., which was equivalent to extrapolating a linear relation between the normalized absorbance at each wavelength and the crystallinity. Groups of bands at 700-800 and 1400-1800 cm⁻¹ were peculiar to the noncryst. spectrum. While there were no easily separated crystalline bands, peaks at 502, 556, and 626 cm⁻¹ were more prominent in the crystalline spectrum.

L2 ANSWER 28 OF 33 CAPLUS COPYRIGHT 2007 ACS on STN

ACCESSION NUMBER: 1980:630306 CAPLUS

DOCUMENT NUMBER: 93:230306

TITLE: Optimization of solvent strength and selectivity for reversed-phase liquid chromatography using an interactive mixture-design statistical technique

AUTHOR(S): Glajch, Joseph L.; Kirkland, J. J.; Squire, Karen M.; Minor, James M.

CORPORATE SOURCE: Cent. Res. Dev. Dep., E. I. du Pont de Nemours and Co., Wilmington, DE, 19898, USA

SOURCE: Journal of Chromatography (1980), 199, 57-79

CODEN: JOCRAM; ISSN: 0021-9673

DOCUMENT TYPE: Journal

LANGUAGE: English

AB A general scheme combines the Snyder solvent selectivity-triangle concept with a mixture-design statistical technique to optimize the strength and selectivity of mobile phase solvents for reversed-phase liquid chromatog. (LC) sepns. In particular, a new method of data anal. called overlapping resolution mapping (ORM) shows advantages over previous chromatog. optimization schemes. The approach can be used to achieve a min. resolution of all components of a mixture or, alternatively, a single pair of several different pairs of compds. within the mixture. In reversed-phase sepns. of 9 naphthalene compds. substituted with different functional groups, tests with MeOH-H₂O, which have significant selectivity differences revealed that no single organic modifier in H₂O could sep. all components. However, when data from 7 separation expts. were analyzed with the interactive computer routine, an optimum solvent mixture was predicted that subsequently gave complete isocratic separation of all components. While anticipated selectivity changes were found with aqueous mixts. of single organic solvents, aqueous binary or ternary mixts. of these organic solvents exhibited anomalous behavior toward certain solutes. In addition, individual solvent strengths were sometimes different from those predicted by previous studies. Tests on a literature LC data set by using simulated solvent mixts. with 15 compds., some exhibiting peak crossovers with different solvent mobile phases, clearly

demonstrated the advantages of the mixture-design ORM method over other chromatog. optimization techniques.

L2 ANSWER 30 OF 33 CAPLUS COPYRIGHT 2007 ACS on STN

ACCESSION NUMBER: 1971:410141 CAPLUS

DOCUMENT NUMBER: 75:10141

TITLE: Analytic self-consistent-field wave functions for the (3d)(4s) configuration of the transition-metal ions

AUTHOR(S): Minor, James M.; Mires, Raymond W.

CORPORATE SOURCE: Dep. Phys., Texas Technol. Univ., Lubbock, TX, USA

SOURCE: Physical Review A: Atomic, Molecular, and Optical Physics (1971), [3]3(6), 1937-8
CODEN: PLRAAN; ISSN: 1050-2947

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The Roothaan method has been used to calculate analytic self-consistent-field functions for the excited (3d)(4s) configuration for the 1st-row transition-metal ions which normally have a (3d)2 ground configuration. Wave functions are calculated for both 1D and 3D multiplets arising from the excited configuration. The sepns. of these 2 multiplet levels from the ground (3d)2 3F level deviate from experiment by 3-8%.

L2 ANSWER 31 OF 33 CAPLUS COPYRIGHT 2007 ACS on STN

ACCESSION NUMBER: 1970:70721 CAPLUS

DOCUMENT NUMBER: 72:70721

ORIGINAL REFERENCE NO.: 72:12935a,12938a

TITLE: Variational calculation of the multiplet spacings in the (3d)2 electron configurations

AUTHOR(S): Minor, James M.; Mires, Raymond W.

CORPORATE SOURCE: Dep. of Phys., Texas Technol. Coll., Lubbock, TX, USA

SOURCE: Physical Review (1970), 189(1), 14-17
CODEN: PHRVAO; ISSN: 0031-899X

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The effect of spatial correlation of the 2 valence electrons on the multiplet spacings has been investigated for atoms with the (1s)2(2s)2-(2p)6(3s)2(3p)6(3d)2 ground configuration. The atom is taken as a two-electron system with each electron moving in a Hartree-Fock effective potential. The zeroth-order wave function is taken to be a Clebsch-Gordan combination of products of one-electron Hartree-Fock orbitals. A variational function of the form $1 + cr_1^2 + c'(r_1 - r_2)^2$ is inserted into this wave function for each of the multiplet members, and c and c' are determined by the variational method. When unrestricted Hartree-Fock functions are used as the zeroth-order basis set, good results which are insensitive to c' are obtained for the multiplet spacings. The 1G-3F spacing is overcorrected by .apprx.-12% compared to +23% without correlation, while the 1D-3F spacing is overcorrected by -3% compared to +34% without correlation.

L2 ANSWER 32 OF 33 CAPLUS COPYRIGHT 2007 ACS on STN

ACCESSION NUMBER: 1971:103200 CAPLUS

DOCUMENT NUMBER: 74:103200

ORIGINAL REFERENCE NO.: 74:16779a,16782a

TITLE: Two-electron correlation effects in Hartree-Fock atomic systems

AUTHOR(S): Minor, James M.

CORPORATE SOURCE: Texas Tech. Univ., Lubbock, TX, USA

SOURCE: (1969) 194 pp. Avail.: Univ. Microfilms, Ann Arbor, Mich., Order No. 70-12,322
From: Diss. Abstr. Int. B 1970, 31(1), 324

DOCUMENT TYPE: Dissertation

LANGUAGE: English

AB Unavailable

L2 ANSWER 33 OF 33 CAPLUS COPYRIGHT 2007 ACS on STN

ACCESSION NUMBER: 1969:505396 CAPLUS

DOCUMENT NUMBER: 71:105396

ORIGINAL REFERENCE NO.: 71:19673a,19676a

TITLE: Variational calculation of the multiplet spacings in the carbon isoelectronic sequence

AUTHOR(S): Minor, James M.; Mires, Raymond W.

CORPORATE SOURCE: Texas Technol. Coll., Lubbock, TX, USA

SOURCE: Physical Review (1969), 185(1), 16-21

CODEN: PHRVAO; ISSN: 0031-899X

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The electron configuration $(1s)2(2s)2(2p)2$ has been treated as a 2-electron problem with the outer 2 electrons moving in the central field produced by the spherically symmetric $(1s)2(2s)2$ charge clouds. The zeroth-order wave function is taken to be a Clebsch-Gordan combination of products of 1-electron Hartree-Fock orbitals. This wave function is then multiplied by a variational function of the form $1 + cr_{12}$ and $1 + cr_{12} + c'(r_1 - r_2)^2$ where c and c' are determined by using the variational principle for each of the 3 multiplet levels. The amount by which the energy is lowered is added to the Hartree-Fock energies to obtain total energies, but it is the ratio of the multiplet spacings which is the main concern. The exptl. value for this ratio is about constant and equal to approx. 1.13 for the sequence C through Ar. The Hartree-Fock ratio ranges from 1.43 for C to 1.49 for Ar. The technique used here gives a ratio which ranges from 1.10 for C to 1.37 for Ar which is in good agreement with experiment even though 2s-2p correlations have been neglected.

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E MINOR JAMES/AU

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E MINOR JAMES M?/AU

L2 33 DUP REM L1 (6 DUPLICATES REMOVED)

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LOGINID:SSSPTA1639MLS

PASSWORD:APRMLS18

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	0.00	-10.92

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E1	3	WOO WILBUR W/AU
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E3	0 -->	WOO WILSO?/AU
E4	2	WOO WILSON/AU
E5	1	WOO WING K/AU
E6	10	WOO WING KEUNG/AU
E7	1	WOO WON BUM/AU
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E9	1	WOO WON HEE/AU
E10	63	WOO WON HONG/AU
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L3 2 "WOO WILSON"/AU

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PROCESSING COMPLETED FOR L3

L4 2 DUP REM L3 (0 DUPLICATES REMOVED)

=> d ibib abs l4 1-2

L4 ANSWER 1 OF 2 CAPLUS COPYRIGHT 2007 ACS on STN
ACCESSION NUMBER: 2005:1335580 CAPLUS
DOCUMENT NUMBER: 144:46258
TITLE: Treatment discovery based on comparative genomic
hybridization (CGH) analysis
INVENTOR(S): Minor, James M.; Woo, Wilson
PATENT ASSIGNEE(S): USA
SOURCE: U.S. Pat. Appl. Publ., 20 pp., Cont.-in-part of U.S.
Ser. No. 640,081.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2005282227	A1	20051222	US 2005-215483	20050830
US 2005037363	A1	20050217	US 2003-640081	20030813
PRIORITY APPLN. INFO.:			US 2003-640081	A2 20030813
AB	Methods, systems and computer readable media for discovering a combination of treatments to reduce the progress of, or eliminate a tissue malady, are			

provided. The methods include the steps of: (a) measuring gene expression values of sample of tissue exhibiting the tissue malady and reference sample tissue that does not exhibit the malady, using CGH array designed to measure gene sequences and possible variations in gene sequences attributable to the malady; (b) generating gene expression signatures from differential expression values of ratios of the measured gene expression values between the sample exhibiting the malady and the reference sample, across all samples, resp.; (c) treating the tissue sample exhibiting the malady with a treatment; (d) measuring a treatment-response value with respect to each of the tissue samples treated, as effected by the treatment; (e) generating a phenotypic signature representing the treatment-response values of each of the tissue samples treated; (f) repeating steps (c)-(e) with a different treatment so that multiple phenotypic signatures have been generated for multiple treatments; (g) performing a clustering operation based on the gene expression signatures of the differential expression levels and the phenotypic signatures of the treatment-response values together; and (h) selecting treatments by identifying the treatment-response phenotypic signatures caused by those treatments. In addition, embodiments of the present invention further relate to computer readable media or computer program products that include program instructions and/or data (including data structures) for performing various computer-implemented operations. The present invention is a forward-looking way of choosing and predicting specific combinations of treatments to test, e.g., using high-throughput (HTP) screening of treatment combinations, and as such, greatly reduces the time to finding successful combinations, which currently have only been discovered accidentally, through hindsight and experiences gained through individual treatments. The treatments identified are targeted to the genes involved in the disease process/malady. Because of this, the chances of significant side effects are reduced. A technique for excluding potential treatments may also be carried out. One example of such an exclusion technique is to generate phenotypic signature representing treatment-response values of each of the tissue samples exhibiting the malady, resultant from treating the tissue samples exhibiting the malady, with treatment having known undesirable characteristics (e.g., is toxic to normal tissues, or ineffective, or has other undesirable side effects, etc.) for treatment of the tissues exhibiting the malady, using the techniques described above.

L4 ANSWER 2 OF 2 CAPLUS COPYRIGHT 2007 ACS on STN

ACCESSION NUMBER: 1986:508777 CAPLUS

DOCUMENT NUMBER: 105:108777

TITLE: Purification and characterization of an FSH releasing protein from porcine ovarian follicular fluid

AUTHOR(S): Vale, Wylie; Rivier, Jean; Vaughan, Joan; McClintock, Richard; Corrigan, Anne; Woo, Wilson; Karr, David; Spiess, Joachim

CORPORATE SOURCE: Clayton Found. Lab. Pept. Biol., Salk Inst., La Jolla, CA, 92037, USA

SOURCE: Nature (London, United Kingdom) (1986), 321(6072), 776-9

CODEN: NATUAS; ISSN: 0028-0836

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The FSH-releasing protein (inhibin BA-chain homodimer) (FRP) [100631-25-2] was purified by HPLC and cation-exchange chromatog. and characterized by SDS-PAGE under reducing and nonreducing conditions and by partial sequence anal. The porcine gonadal FRP is a homopolymer of 2 inhibin BA-chains linked by SS bonds. FRP is potent with a median ID of .apprx.25 pM for stimulating FSH [9002-68-0] secretion and biosynthesis. No other pituitary hormones were stimulated by FRP and in contrast to LH-RH and other gonadal gonadotropin-releasing fractions it is not mediated by LH-RH receptors.

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COST IN U.S. DOLLARS

SINCE FILE	TOTAL
ENTRY	SESSION
17.71	119.01

FULL ESTIMATED COST

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)

SINCE FILE	TOTAL
ENTRY	SESSION
-1.56	-12.48

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